



1600

RAW SEQUENCE LISTING

DATE: 09/20/2004

PATENT APPLICATION: US/09/456,306A

TIME: 16:09:01

Input Set : A:\021123-0265182.ST25.txt

Output Set: N:\CRF4\09202004\I456306A.raw

3 <110> APPLICANT: DEGUSSA AG
 5 <120> TITLE OF INVENTION: NOVEL NUCLEOTIDE SEQUENCES CODING FOR THE poxB GENE
 7 <130> FILE REFERENCE: 021123-0265182
 9 <140> CURRENT APPLICATION NUMBER: US 09/456,306A
 10 <141> CURRENT FILING DATE: 1999-12-08
 12 <150> PRIOR APPLICATION NUMBER: DE 199 51 975.7
 13 <151> PRIOR FILING DATE: 1999-10-28
 15 <160> NUMBER OF SEQ ID NOS: 5
 17 <170> SOFTWARE: PatentIn version 3.3
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2160
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Corynebacterium glutamicum
 25 <220> FEATURE:
 26 <221> NAME/KEY: -35_signal
 27 <222> LOCATION: (227)..(232)
 29 <220> FEATURE:
 30 <221> NAME/KEY: -10_signal
 31 <222> LOCATION: (256)..(261)
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (327)..(2063)
 37 <400> SEQUENCE: 1
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 40 cgaggcgacc agacaggcgt gcccacgatg tttaaataagg cgatcgggtg gcatctgtgt 120
 42 ttggtttcga cgggctgaaa ccaaaccaga ctgcccagca acgacggaaa tcccaaaagt 180
 44 gggcatccct gtttggtacc gagtaccac cggggcctga aactccctgg caggcgggcg 240
 46 aagcgtggca acaactggaa tttaagagca caattgaagt cgcaccaagt taggcaacac 300
 48 aatagccata acgttgagga gttcag atg gca cac agc tac gca gaa caa tta 353
 49 Met Ala His Ser Tyr Ala Glu Gln Leu
 50 1 5
 52 att gac act ttg gaa gct caa ggt gtg aag cga att tat ggt ttg gtg 401
 53 Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val
 54 10 15 20 25
 56 ggt gac agc ctt aat ccg atc gtg gat gct gtc cgc caa tca gat att 449
 57 Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg Gln Ser Asp Ile
 58 30 35 40
 60 gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg ttt gca gcc ggt 497
 61 Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala Phe Ala Ala Gly
 62 45 50 55
 64 gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt gct gct tct tgt 545
 65 Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys
 66 60 65 70



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68 ggt cct gga aac aca cac ctg att cag ggt ctt tat gat tcg cat cga      593
69 Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr Asp Ser His Arg
70      75      80      85
72 aat ggt gcg aag gtg ttg gcc atc gct agc cat att ccg agt gcc cag      641
73 Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile Pro Ser Ala Gln
74 90      95      100      105
76 att ggt tcg acg ttc ttc cag gaa acg cat ccg gag att ttg ttt aag      689
77 Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu Ile Leu Phe Lys
78      110      115      120
80 gaa tgc tct ggt tac tgc gag atg gtg aat ggt ggt gag cag ggt gaa      737
81 Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly Glu Gln Gly Glu
82      125      130      135
84 cgc att ttg cat cac gcg att cag tcc acc atg gcg ggt aaa ggt gtg      785
85 Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala Gly Lys Gly Val
86      140      145      150
88 tcg gtg gta gtg att cct ggt gat atc gct aag gaa gac gca ggt gac      833
89 Ser Val Val Val Ile Pro Gly Asp Ile Ala Lys Glu Asp Ala Gly Asp
90      155      160      165
92 ggt act tat tcc aat tcc act att tct tct ggc act cct gtg gtg ttc      881
93 Gly Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr Pro Val Val Phe
94 170      175      180      185
96 ccg gat cct act gag gct gca gcg ctg gtg gag gcg att aac aac gct      929
97 Pro Asp Pro Thr Glu Ala Ala Ala Leu Val Glu Ala Ile Asn Asn Ala
98      190      195      200
100 aag tct gtc act ttg ttc tgc ggt gcg ggc gtg aag aat gct cgc gcg      977
101 Lys Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys Asn Ala Arg Ala
102      205      210      215
104 cag gtg ttg gag ttg gcg gag aag att aaa tca ccg atc ggg cat gcg      1025
105 Gln Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro Ile Gly His Ala
106      220      225      230
108 ctg ggt ggt aag cag tac atc cag cat gag aat ccg ttt gag gtc ggc      1073
109 Leu Gly Gly Lys Gln Tyr Ile Gln His Glu Asn Pro Phe Glu Val Gly
110      235      240      245
112 atg tct ggc ctg ctt ggt tac ggc gcc tgc gtg gat gcg tcc aat gag      1121
113 Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp Ala Ser Asn Glu
114 250      255      260      265
116 gcg gat ctg ctg att cta ttg ggt acg gat ttc cct tat tct gat ttc      1169
117 Ala Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro Tyr Ser Asp Phe
118      270      275      280
120 ctt cct aaa gac aac gtt gcc cag gtg gat atc aac ggt gcg cac att      1217
121 Leu Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn Gly Ala His Ile
122      285      290      295
124 ggt cga cgt acc acg gtg aag tat ccg gtg acc ggt gat gtt gct gca      1265
125 Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly Asp Val Ala Ala
126      300      305      310
128 aca atc gaa aat att ttg cct cat gtg aag gaa aaa aca gat cgt tcc      1313
129 Thr Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys Thr Asp Arg Ser
130      315      320      325
132 ttc ctt gat cgg atg ctc aag gca cac gag cgt aag ttg agc tcg gtg      1361

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133	Phe	Leu	Asp	Arg	Met	Leu	Lys	Ala	His	Glu	Arg	Lys	Leu	Ser	Ser	Val	
134	330					335					340					345	
136	gta	gag	acg	tac	aca	cat	aac	gtc	gag	aag	cat	gtg	cct	att	cac	cct	1409
137	Val	Glu	Thr	Tyr	Thr	His	Asn	Val	Glu	Lys	His	Val	Pro	Ile	His	Pro	
138					350					355					360		
140	gaa	tac	gtt	gcc	tct	att	ttg	aac	gag	ctg	gcg	gat	aag	gat	gcg	gtg	1457
141	Glu	Tyr	Val	Ala	Ser	Ile	Leu	Asn	Glu	Leu	Ala	Asp	Lys	Asp	Ala	Val	
142				365					370					375			
144	ttt	act	gtg	gat	acc	ggc	atg	tgc	aat	gtg	tgg	cat	gcg	agg	tac	atc	1505
145	Phe	Thr	Val	Asp	Thr	Gly	Met	Cys	Asn	Val	Trp	His	Ala	Arg	Tyr	Ile	
146			380					385					390				
148	gag	aat	ccg	gag	gga	acg	cgc	gac	ttt	gtg	ggt	tca	ttc	cgc	cac	ggc	1553
149	Glu	Asn	Pro	Glu	Gly	Thr	Arg	Asp	Phe	Val	Gly	Ser	Phe	Arg	His	Gly	
150		395					400				405						
152	acg	atg	gct	aat	gcg	ttg	cct	cat	gcg	att	ggt	gcg	caa	agt	gtt	gat	1601
153	Thr	Met	Ala	Asn	Ala	Leu	Pro	His	Ala	Ile	Gly	Ala	Gln	Ser	Val	Asp	
154	410				415				420							425	
156	cga	aac	cgc	cag	gtg	atc	gcg	atg	tgt	ggc	gat	ggt	ggt	ttg	ggc	atg	1649
157	Arg	Asn	Arg	Gln	Val	Ile	Ala	Met	Cys	Gly	Asp	Gly	Gly	Leu	Gly	Met	
158				430					435						440		
160	ctg	ctg	ggt	gag	ctt	ctg	acc	gtt	aag	ctg	cac	caa	ctt	ccg	ctg	aag	1697
161	Leu	Leu	Gly	Glu	Leu	Leu	Thr	Val	Lys	Leu	His	Gln	Leu	Pro	Leu	Lys	
162				445					450					455			
164	gct	gtg	gtg	ttt	aac	aac	agt	tct	ttg	ggc	atg	gtg	aag	ttg	gag	atg	1745
165	Ala	Val	Val	Phe	Asn	Asn	Ser	Ser	Leu	Gly	Met	Val	Lys	Leu	Glu	Met	
166			460					465					470				
168	ctc	gtg	gag	gga	cag	cca	gaa	ttt	ggt	act	gac	cat	gag	gaa	gtg	aat	1793
169	Leu	Val	Glu	Gly	Gln	Pro	Glu	Phe	Gly	Thr	Asp	His	Glu	Glu	Val	Asn	
170		475				480					485						
172	ttc	gca	gag	att	gcg	gcg	gct	gcg	ggt	atc	aaa	tcg	gta	cgc	atc	acc	1841
173	Phe	Ala	Glu	Ile	Ala	Ala	Ala	Ala	Gly	Ile	Lys	Ser	Val	Arg	Ile	Thr	
174	490				495				500						505		
176	gat	ccg	aag	aaa	gtt	cgc	gag	cag	cta	gct	gag	gca	ttg	gca	tat	cct	1889
177	Asp	Pro	Lys	Lys	Val	Arg	Glu	Gln	Leu	Ala	Glu	Ala	Leu	Ala	Tyr	Pro	
178				510					515						520		
180	gga	cct	gta	ctg	atc	gat	atc	gtc	acg	gat	cct	aat	gcg	ctg	tcg	atc	1937
181	Gly	Pro	Val	Leu	Ile	Asp	Ile	Val	Thr	Asp	Pro	Asn	Ala	Leu	Ser	Ile	
182				525					530					535			
184	cca	cca	acc	atc	acg	tgg	gaa	cag	gtc	atg	gga	ttc	agc	aag	gcg	gcc	1985
185	Pro	Pro	Thr	Ile	Thr	Trp	Glu	Gln	Val	Met	Gly	Phe	Ser	Lys	Ala	Ala	
186			540					545					550				
188	acc	cga	acc	gtc	ttt	ggt	gga	gga	gta	gga	gcg	atg	atc	gat	ctg	gcc	2033
189	Thr	Arg	Thr	Val	Phe	Gly	Gly	Gly	Val	Gly	Ala	Met	Ile	Asp	Leu	Ala	
190		555				560					565						
192	cgt	tcg	aac	ata	agg	aat	att	cct	act	cca	tgatgattga	tacacctgct				2083	
193	Arg	Ser	Asn	Ile	Arg	Asn	Ile	Pro	Thr	Pro							
194	570					575											
196	gttctcattg	accgcgagcg	cttaactgcc	aacatttcca	ggatggcagc	tcacgccggt										2143	
198	gcccattgaga	ttgccct														2160	

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201 <210> SEQ ID NO: 2
202 <211> LENGTH: 579
203 <212> TYPE: PRT
204 <213> ORGANISM: Corynebacterium glutamicum
206 <400> SEQUENCE: 2
208 Met Ala His Ser Tyr Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln
209 1 5 10 15
212 Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile
213 20 25 30
216 Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn
217 35 40 45
220 Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
221 50 55 60
224 Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
225 65 70 75 80
228 Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
229 85 90 95
232 Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
233 100 105 110
236 Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
237 115 120 125
240 Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
241 130 135 140
244 Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Ile Pro Gly
245 145 150 155 160
248 Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr
249 165 170 175
252 Ile Ser Ser Gly Thr Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala
253 180 185 190
256 Ala Leu Val Glu Ala Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys
257 195 200 205
260 Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu
261 210 215 220
264 Lys Ile Lys Ser Pro Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile
265 225 230 235 240
268 Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr
269 245 250 255
272 Gly Ala Cys Val Asp Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu
273 260 265 270
276 Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
277 275 280 285
280 Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
281 290 295 300
284 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
285 305 310 315 320
288 His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
289 325 330 335
292 Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
293 340 345 350

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296 Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
297           355           360           365
300 Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
301           370           375           380
304 Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
305 385           390           395           400
308 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
309           405           410           415
312 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
313           420           425           430
316 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
317           435           440           445
320 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
321           450           455           460
324 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
325 465           470           475           480
328 Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
329           485           490           495
332 Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
333           500           505           510
336 Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
337           515           520           525
340 Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
341           530           535           540
344 Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
345 545           550           555           560
348 Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile
349           565           570           575

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352 Pro Thr Pro

356 <210> SEQ ID NO: 3

357 <211> LENGTH: 875

358 <212> TYPE: DNA

359 <213> ORGANISM: Corynebacterium glutamicum

361 <400> SEQUENCE: 3

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364 accatggcgg gtaaaagggt gtcgggtggta gtgattcctg gtgatatcgc taaggaagac 120
366 gcaggtgacg gtacttattc caattccact atttcttctg gcactcctgt ggtgttcccg 180
368 gatcctactg aggctgcagc gctggtggag gcgattaaca acgctaagtc tgtcactttg 240
370 ttctgcgggt cgggcgtgaa gaatgctcgc gcgcagggtg tggagttggc ggagaagatt 300
372 aaatcaccca tcgggcatgc gctgggtggg aagcagtaca tccagcatga gaatccgttt 360
374 gaggtcggca tgtctggcct gcttggttac ggcgcctgcg tggatgcgtc caatgaggcg 420
376 gatctgctga ttctattggg tacggatttc cettattctg atttccttcc taaagacaac 480
378 gttgcccagg tggatatcaa cggtgcgcac attggtcgac gtaccacggg gaagtatccg 540
380 gtgaccgggt atgttgctgc aacaatcgaa aatattttgc ctcatgtgaa ggaaaaaaca 600
382 gatcgttcct tccttgatcg gatgctcaag gcacacgagc gtaagttgag ctcggtggta 660
384 gagacgtaca cacataacgt cgagaagcat gtgcctattc accctgaata cgttgccctc 720
386 attttgaacg agctggcgga taaggatgcg gtgtttactg tggataccgg catgtgcaat 780
388 gtgtggcatg cgaggtacat cgagaatccg gagggaacgc gcgactttgt gggttcattc 840
390 cgccacggca cgatggctaa tgcgttgccct catgc 875

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:4,5

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